



SEQUENCE LISTING

<210> STRACKE, MARY
LIOTTA, LANCE
SCHIFFMANN, ELLIOTT
KRUTZCH, HENRY
MURATA, JUN

<120> AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
CANCER DIAGNOSIS AND THERAPY

<130> 2026-4149US4

<140> 09/483,831

<141> 2000-01-17

<150> 07/822,043

<151> 1992-01-17

<150> 08/249,182

<151> 1994-05-25

<150> 08/346,455

<151> 1994-11-28

<150> 08/977,221

<151> 1997-11-24

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<170> PatentIn Ver. 2.1

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Gln Ala Glu Val Ser
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<210> 24

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<222> (16)

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<221> variation

<222> (39)

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<210> 26

<211> 9

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<223> Description of Artificial Sequence: Synthetic
Peptide

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<210> 27

<211> 5

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<223> Description of Artificial Sequence: Synthetic
Peptide

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Val Leu Asn Tyr Phe

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<210> 28

<211> 5

<212> PRT

<213> Artificial Sequence

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Tyr Leu Asn Ala Thr

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<210> 29

<211> 11

<212> PRT

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Peptide

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His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr

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Ser Tyr Pro Glu Ile Leu Thr Pro Ala Asp Asn

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Peptide

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His Asp Thr Glu Asp Lys
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<213> Homo sapiens

<220>
<223> Putative protein sequence of A2058 Autotoxin

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Cys His Asp Phe Asp Glu Leu Cys Leu Lys Thr Ala Arg Gly Trp Glu
1 5 10 15

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His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly	Asp	Cys	Cys	Thr	Asn	Tyr			
		35					40					45						
Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp	Val	Asp	Asp	Asp	Cys	Glu			
	50					55					60							
Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	Ala	Gly	Phe	Val	Arg	Pro	Pro	Leu			
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Ile	Ile	Phe	Ser	Val	Asp	Gly	Phe	Arg	Ala	Ser	Tyr	Met	Lys	Lys	Gly			
				85				90						95				
Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu	Arg	Ser	Cys	Gly	Thr	His			
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Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	Pro	Thr	Lys	Thr	Phe	Pro	Asn	Leu			
		115					120					125						
Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile	Val	Gly			
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Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	Thr	Phe	His	Leu	Arg	Gly			
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Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly	Gly	Gln	Pro	Leu	Trp	Ile			
				165					170					175				
Thr	Ala	Thr	Lys	Gln	Gly	Val	Lys	Ala	Gly	Thr	Phe	Phe	Trp	Ser	Val			
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Val	Ile	Pro	His	Glu	Arg	Arg	Ile	Leu	Thr	Ile	Leu	Arg	Trp	Leu	Thr			
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Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	Val	Tyr	Ala	Phe	Tyr	Ser	Glu	Gln			
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Ser	Tyr	Gly	Ser	Pro	Phe	Thr	Pro	Ala	Lys	Arg	Pro	Lys	Arg	Lys	Val			
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Ala	Pro	Lys	Arg	Arg	Gln	Glu	Arg	Pro	Val	Ala	Pro	Pro	Lys	Lys	Arg			
			260				265						270					

Arg	Arg	Lys	Ile	His	Arg	Met	Asp	His	Tyr	Ala	Ala	Glu	Thr	Arg	Gln	275	280	285	
Asp	Lys	Met	Thr	Asn	Pro	Leu	Arg	Glu	Ile	Asp	Lys	Ile	Val	Gly	Gln	290	295	300	
Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	Arg	Arg	Cys	Val	Asn	Val	305	310	315	320
Ile	Phe	Val	Gly	Asp	His	Gly	Met	Glu	Asp	Val	Thr	Cys	Asp	Arg	Thr	325	330	335	
Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu	Val	340	345	350	
Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala	Lys	355	360	365	
Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro	Asp	370	375	380	
Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu	His	385	390	395	400
Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu	Arg	405	410	415	
Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro	Ser	420	425	430	
Gly	Lys	Cys	Phe	Phe	Gln	Gly	Asp	His	Gly	Phe	Asp	Asn	Lys	Val	Asn	435	440	445	
Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr	Lys	450	455	460	
Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met	Cys	465	470	475	480
Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly	Ser	485	490	495	
Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro	Glu	500	505	510	
Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser	Asp	515	520	525	

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Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn	Asp	Lys
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Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser	Ser	Pro
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Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro	Met	Tyr
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Pro	Ala	Phe	Lys	Arg	Val	Trp	Asn	Tyr	Phe	Gln	Arg	Val	Leu	Val	Lys
	675						680						685		
Lys	Tyr	Ala	Ser	Glu	Arg	Asn	Gly	Val	Asn	Val	Ile	Ser	Gly	Pro	Ile
690						695					700				
Phe	Asp	Tyr	Asp	Tyr	Asp	Gly	Leu	His	Asp	Thr	Glu	Asp	Lys	Ile	Lys
705					710					715				720	
Gln	Tyr	Val	Glu	Gly	Ser	Ser	Ile	Pro	Val	Pro	Thr	His	Tyr	Tyr	Ser
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Ile	Ile	Thr	Ser	Cys	Leu	Asp	Phe	Thr	Gln	Pro	Ala	Asp	Lys	Cys	Asp
			740						745				750		
Gly	Pro	Leu	Ser	Val	Ser	Ser	Phe	Ile	Leu	Pro	His	Arg	Pro	Asp	Asn
	755						760					765			
Glu	Glu	Ser	Cys	Asn	Ser	Ser	Glu	Asp	Glu	Ser	Lys	Trp	Val	Glu	Glu
770						775					780				

Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His Leu Thr
 785 790 795 800

Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu
 805 810 815

Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile
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<211> 2946

<212> DNA

<213> Homo sapiens

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<223> Partial DNA sequence of A2058 Autotoxin

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<210> 36

<211> 788

<212> PRT

<213> Homo sapiens

<220>

<223> N-tera 2D1 putative ATX protein sequence

<400> 36

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Cys Asp Asn Leu Cys Lys Ser Tyr Thr Ser Cys Cys His Asp Phe Asp
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Glu Leu Cys Leu Lys Thr Ala Arg Ala Trp Glu Cys Thr Lys Asp Arg
      20              25              30

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```

Cys Gly Glu Val Arg Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp
      35              40              45

```

```

Cys Leu Ala Arg Gly Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys
      50              55              60

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Gly Glu Ser His Trp Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala
      65              70              75              80

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Glu Cys Leu Gln Val Asp Ser Pro Ser Ile Asn His Leu Leu Arg Gly

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85

90

95

Trp Leu Pro Met Thr Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro
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Asn Ile Glu Lys Leu Arg Ser Cys Gly Thr His Ser Pro Tyr Met Arg
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Pro Val Tyr Pro Thr Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr
130 135 140

Gly Leu Tyr Pro Glu Ser His Gly Ile Val Gly Asn Ser Met Tyr Asp
145 150 155 160

Pro Val Phe Asp Ala Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn
165 170 175

His Arg Trp Trp Ala Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln
180 185 190

Arg Gly Glu Ser Trp Asn Ile Leu Leu Val Cys Cys His Pro Ser Arg
195 200 205

Ala Glu Ile Leu Thr Ile Leu Gln Trp Leu Thr Leu Pro Asp His Glu
210 215 220

Arg Pro Ser Val Tyr Ala Phe Tyr Ser Glu Gln Pro Asp Phe Ser Gly
225 230 235 240

His Lys His Met Pro Phe Gly Pro Glu Met Pro Asn Pro Leu Arg Glu
245 250 255

Met His Lys Ile Val Gly Gln Leu Met Asp Gly Leu Lys Gln Leu Lys
260 265 270

Leu His Arg Cys Val Asn Val Ile Phe Val Glu Thr Met Asp Gly Arg
275 280 285

Cys His Met Tyr Arg Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val
290 295 300

Asp Asp Ile Thr Leu Val Pro Gly Thr Leu Gly Arg Ile Arg Ser Lys
305 310 315 320

Phe Ser Asn Asn Ala Lys Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu
325 330 335

Thr Cys Lys Lys Pro Asp Gln His Phe Lys Pro Tyr Leu Lys Gln His

340

345

350

Leu Pro Lys Arg Leu His Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile
355 360 365

His Leu Leu Val Glu Arg Arg Trp His Val Ala Arg Lys Pro Leu Asp
370 375 380

Val Tyr Lys Lys Pro Ser Gly Asn Ala Phe Ser Arg Glu Thr Thr Ala
385 390 395 400

Phe Asp Asn Lys Val Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly
405 410 415

Pro Thr Phe Lys Tyr Lys Thr Lys Val Pro Pro Phe Glu Asn Ile Glu
420 425 430

Leu Tyr Asn Val Met Cys Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn
435 440 445

Asn Gly Thr His Phe Ser Leu Asn His Leu Leu Arg Thr Asn Thr Phe
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Arg Pro Thr Met Pro Glu Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile
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Met Tyr Leu Gln Ser Asp Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys
485 490 495

Val Glu Pro Lys Asn Lys Leu Asp Glu Leu Asn Lys Arg Leu His Thr
500 505 510

Lys Gly Ser Thr Glu Glu Arg His Leu Leu Tyr Gly Asp Arg Pro Ala
515 520 525

Val Leu Tyr Arg Thr Arg Tyr Asp Ile Leu Tyr His Thr Asp Phe Glu
530 535 540

Ser Gly Tyr Ser Glu Ile Phe Leu Met Pro Leu Trp Thr Ser Tyr Thr
545 550 555 560

Val Ser Lys Gln Ala Glu Val Ser Ser Val Pro Asp His Leu Thr Ser
565 570 575

Cys Val Arg Pro Asp Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys
580 585 590

Leu Ala Tyr Lys Asn Asp Lys Gln Met Ser Tyr Gly Gly Leu Gly Pro

595

600

605

Pro Tyr Leu Ser Ser Ser Pro Glu Ala Lys Tyr Asp Ala Phe Leu Val
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Thr Asn Met Val Pro Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr
 625 630 635 640

Phe Gln Arg Val Leu Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val
 645 650 655

Asn Val Ile Ser Gly Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His
 660 665 670

Asp Thr Glu Asp Lys Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro
 675 680 685

Val Pro Thr His Tyr Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr
 690 695 700

Gln Pro Ala Asp Lys Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile
 705 710 715 720

Leu Pro His Arg Pro Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp
 725 730 735

Glu Ser Lys Trp Val Glu Glu Leu Met Lys Met His Thr Ala Arg Val
 740 745 750

Arg Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser
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Arg Ser Tyr Pro Glu Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr
 770 775 780

Glu Ser Glu Ile
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<210> 37

<211> 2712

<212> DNA

<213> Homo sapiens

<220>

<223> N-tera 2D1 ATX DNA sequence

<400> 37

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<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: Synthetic
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<400> 38
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<210> 39
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 39
Met His Thr Ala Arg Val Arg Asp
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<210> 40
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Peptide

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Phe Ser Asn Asn Ala Lys Tyr Asp
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<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 41

Val Met Pro Asn Ile Glu Lys

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<210> 42

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 42

Thr Ala Arg Gly Trp Glu Cys Thr

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<210> 43

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Peptide

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<222> (1)

<223> Xaa represents either an unknown or any amino acid
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<220>

<221> VARIANT

<222> (7)

<400> 43

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5

10

<210> 44
<211> 11
<212> PRT
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Peptide

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<210> 45
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<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 45
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<210> 46
<211> 13
<212> PRT
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Peptide

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<210> 47
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Peptide

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Ile Val Gly Gln Leu Met Asp Gly

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5

<210> 48

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 48

Thr Ser Arg Ser Tyr Pro Glu Ile Leu

1

5

<210> 49

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 49

Gln Ala Glu Val Ser Ser Val Pro Asp

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5

<210> 50

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 50

Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro Asp Asp Cys

1

5

10

<210> 51
<211> 12
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic Peptide

<400> 51
Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu
1 5 10

<210> 52
<211> 16
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic Peptide

<400> 52
Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro
1 5 10 15

<210> 53
<211> 117
<212> DNA
<213> Homo sapiens

<220>

<223> 5' end of human liver ATX gene

<400> 53
atggcaagga ggagctcggt ccagtcgtgt caagatatat ccctgttcac ttttgccggt 60
ggagtcaata tctgcttagg attcactgca catcgaatta agagagcaga aggatgg 117

<210> 54
<211> 39
<212> PRT
<213> Homo sapiens

<220>

<223> N-terminal region including transmembrane domain
of liver ATX protein

<400> 54

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp Ile Ser Leu Phe
1 5 10 15

Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg
20 25 30

Ile Lys Arg Ala Glu Gly Trp
35

<210> 55

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 55

gctcagataa ggaggaaaga g

21

<210> 56

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 56

gaatccgtag gacatctgct t

21

<210> 57

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

Primer

<400> 57
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21

<210> 58
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

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<223> Base y represents t/u or c.

<220>
<221> variation
<222> (6)
<223> Base n represents inosine.

<220>
<221> variation
<222> (12)
<223> Base r represents g or a.

<220>
<221> variation
<222> (15)
<223> Base n represents inosine.

<220>
<221> variation
<222> (18)
<223> Base n represents inosine.

<220>
<221> variation
<222> (21)
<223> Base y represents c or t/u.

<220>
<221> variation
<222> (24)

<223> Base n represents inosine.

<400> 58

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25

<210> 59

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

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<222> (3)

<223> Base y represents c or t/u.

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<221> variation

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<221> variation

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<223> Base n represents inosine.

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<221> variation

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<221> variation

<222> (24)

<223> Base y represents c or t/u.

<400> 59

ttygtnggnt ayggncnac nttyaa

26

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

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<222> (3)

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<221> variation

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<223> Base y represents c or t/u.

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<221> variation

<222> (18)

<223> Base n represents inosine.

<220>

<221> variation

<222> (21)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (24)

<223> Base y represents c or t/u.

<400> 60

aaytayctna cnaaygtnga ygayat

26

<210> 61

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

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<222> (3)

<223> Base y represents c or t/u.

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<221> variation

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<223> Base n represents inosine.

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<221> variation

<222> (12)

<223> Base n represents inosine.

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<221> variation

<222> (15)

<223> Base n represents inosine.

<220>

<221> variation

<222> (18)

<223> Base n represents inosine..

<220>

<221> variation

<222> (21)

<223> Base n represents inosine.

<220>

<221> variation

<222> (24)

<223> Base n represents inosine.

<400> 61

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26

<210> 62

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<220>

<221> variation

<222> (3)

<223> Base y represents t/u or c.

<220>

<221> variation

<222> (6)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (9)..(10)

<223> Base r represents a or g. Base y represents c
or t/u.

<220>

<221> variation

<222> (12)
<223> Base n represents inosine.

<220>
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<222> (15)
<223> Base r represents a or g.

<220>
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<222> (18)
<223> Base r represents a or g.

<220>
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<222> (21)
<223> Base n represents inosine.

<220>
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<222> (24)
<223> Base n represents inosine.

<220>
<221> variation
<222> (27)
<223> Base n represents inosine.

<400> 62
tgyttygary tncargargc nggnccncc

29

<210> 63
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Putative autotoxin protein sequence from human
liver

<220>
<221> VARIANT
<222> (860)
<223> Xaa at positions: 860, 889, 905, 911, 927, 937,
944, 950, 954, 967, 975 represents either an
unknown or any amino acid residue.

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 63

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18

<210> 64

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 64

ctgggtggctg taatccatag c

21

<210> 65

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 65

cgtgaaggca aagagaacac g

21

<210> 66

<211> 3104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Polynucleotide

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ttcgggtctat	gccttctatt	ctgagcaacc	tgatttctct	ggacacaaat	atgcctttcg	1020
gccctgagat	gacaaatcct	ctgagggaaa	tcgacaaaat	tgtggggcaa	ttaatggatg	1080
gactgaaaca	actaaaactg	catcgggtgtg	tcaacgtcat	ctttgtcgga	gaccatggaa	1140
tggaagatgt	cacatgtgat	agaactgagt	tcttgagtaa	ttacctaact	aatgtggatg	1200
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gccgcagcta	cccagaaatc	ctgacactca	agacatacct	gcatacatat	gagagcgaga	2640
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aaatctgaca	tattatgcct	gaatgactcc	actgtttttc	tctaattgctt	gatttaggta	2820
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tctaaatggg	gctgcagatt	tgatattttg	attgaggaaa	tattaatttt	ccaatgcaca	2940
gttgccacat	ttagtctgtg	actgtatgga	aacactgatt	ttgtaaagtt	gcctttattt	3000
gctgttaact	gttaactatg	acagatatat	ttaagcctta	taaaccaatc	ttaaacataa	3060
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<210> 67

<211> 861

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Polypeptide

<400> 67

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Ile Ile Ser Leu Phe
1 5 10 15

Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg
20 25 30

Ile Lys Arg Ala Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser
35 40 45

Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys Gly Arg Cys Phe
50 55 60

Glu Leu Gln Glu Ala Gly Pro Pro Asp Cys Arg Cys Asp Asn Leu Cys
65 70 75 80

Lys Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys
85 90 95

Thr Ala Arg Ala Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu Val Arg
100 105 110

Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp Cys Leu Ala Arg Gly
115 120 125

Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp
130 135 140

Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Pro Ala Gly
145 150 155 160

Phe Val Arg Pro Pro Leu Ile Ile Phe Ser Val Asp Gly Phe Arg Ala
165 170 175

Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu
180 185 190

Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	His	Met	Arg	Pro	Val	Tyr	Pro	Thr	195	200	205	
Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	210	215	220	
Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	225	230	235	240
Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly	245	250	255	
Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	Arg	Gly	Glu	Ser	Trp	260	265	270	
Asn	Ile	Leu	Leu	Val	Cys	Cys	His	Pro	Ser	Arg	Ala	Glu	Ile	Leu	Thr	275	280	285	
Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Leu	Arg	Ser	Met	290	295	300	
Pro	Ser	Ile	Leu	Ser	Asn	Leu	Ile	Ser	Leu	Asp	Thr	Asn	Met	Pro	Phe	305	310	315	320
Gly	Pro	Glu	Met	Thr	Asn	Pro	Leu	Arg	Glu	Ile	Asp	Lys	Ile	Val	Gly	325	330	335	
Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	His	Arg	Cys	Val	Asn	340	345	350	
Val	Ile	Phe	Val	Gly	Asp	His	Gly	Met	Glu	Asp	Val	Thr	Cys	Asp	Arg	355	360	365	
Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu	370	375	380	
Val	Pro	Gly	Thr	Leu	Gly	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala	Lys	385	390	395	400
Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro	Asp	405	410	415	
Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu	His	420	425	430	
Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu	Arg	435	440	445	

Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro	Ser	450	455	460	
Gly	Lys	Cys	Phe	Phe	Gln	Gly	Asp	His	Gly	Phe	Asp	Asn	Lys	Val	Asn	465	470	475	480
Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr	Lys	485	490	495	
Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met	Cys	500	505	510	
Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly	Ser	515	520	525	
Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro	Glu	530	535	540	
Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser	Asp	545	550	555	560
Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn	Lys	565	570	575	
Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys	Gly	Ser	Thr	Glu	Glu	580	585	590	
Arg	His	Leu	Leu	Tyr	Gly	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr	Arg	Tyr	595	600	605	
Asp	Val	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu	Ile	Phe	610	615	620	
Leu	Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala	Glu	Val	625	630	635	640
Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp	Val	Arg	645	650	655	
Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn	Asp	Lys	660	665	670	
Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser	Ser	Pro	675	680	685	
Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro	Met	Tyr	690	695	700	

Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu Val Lys
705 710 715 720

Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly Pro Ile
725 730 735

Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys Ile Lys
740 745 750

Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr Tyr Ser
755 760 765

Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys Cys Asp
770 775 780

Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Arg His Arg Pro Asp Asn
785 790 795 800

Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val Glu Glu
805 810 815

Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His Leu Thr
820 825 830

Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu
835 840 845

Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile
850 855 860

<210> 68

<211> 3251

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Polynucleotide

<400> 68

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ctgcttagga ttcactgcac atcgaattaa gagagcagaa ggatgggagg aaggctcctcc 180
tacagtgtca tcagactccc cctggaccaa catctccgga tcttgcaagg gcaggtgctt 240
tgaacttcaa gaggtgtgac ctctgtattg tcgctgtgac aacttgtgta agagctatac 300
cagttgctgc catgactttg atgagctgtg tttgaagaca gcccggtggct gggagtgtac 360
taaggacaga tgtggagaag tcagaaatga agaaaatgcc tgtcactgct cagaggactg 420

ctggccagg ggagactgct gtaccaatta ccaagtgggt tgcaaaggag agtcgcattg 480
 ggttgatgat gactgtgagg aaataaaggc cgcagaatgc cctgcagggt ttgttcgccc 540
 tccattaatc atcttctccg tggatggctt ccgtgcatca tacatgaaga aaggcagcaa 600
 agtcatgcct aatattgaaa aactaaggct ttgtggcaca cactctccct acatgaggcc 660
 ggtgtaccca actaaaacct ttcctaactt atacactttg gccactgggc tatatccaga 720
 atcacatgga attggtggca attcaatgta tgatcctgta tttgatgcca cttttcatct 780
 gcgagggcga gagaaattta atcatagatg gtggggagggt caaccgctat ggattacagc 840
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 gagaatatta accatattgc ggtggctcac cctgccagat catgagaggc cttcgggtcta 960
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 tttgaagcctt ataaaccaat cttaaacata ataaatcaca cattcagttt taaaaaaaaa 3240
 aaaaaaaaaa a 3251

<210> 69
<211> 915
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Polypeptide

<400> 69

Met	Ala	Arg	Arg	Ser	Ser	Phe	Gln	Ser	Cys	Gln	Ile	Ile	Ser	Leu	Phe
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Thr	Phe	Ala	Val	Gly	Val	Ser	Ile	Cys	Leu	Gly	Phe	Thr	Ala	His	Arg
			20					25					30		
Ile	Lys	Arg	Ala	Glu	Gly	Trp	Glu	Glu	Gly	Pro	Pro	Thr	Val	Leu	Ser
	35					40						45			
Asp	Ser	Pro	Trp	Thr	Asn	Ile	Ser	Gly	Ser	Cys	Lys	Gly	Arg	Cys	Phe
	50					55					60				
Glu	Leu	Gln	Glu	Ala	Gly	Pro	Pro	Asp	Cys	Arg	Cys	Asp	Asn	Leu	Cys
	65				70					75				80	
Lys	Ser	Tyr	Thr	Ser	Cys	Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys
				85					90					95	
Thr	Ala	Arg	Gly	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	Val	Arg
		100						105					110		
Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly
	115						120					125			
Asp	Cys	Cys	Thr	Asn	Tyr	Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp
	130					135					140				
Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	Ala	Gly
145				150					155					160	
Phe	Val	Arg	Pro	Pro	Leu	Ile	Ile	Phe	Ser	Val	Asp	Gly	Phe	Arg	Ala
			165					170					175		
Ser	Tyr	Met	Lys	Lys	Gly	Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu
	180						185						190		

Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	Pro	Thr	195	200	205	
Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	210	215	220	
Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	225	230	235	240
Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly	245	250	255	
Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	Gly	Val	Lys	Ala	Gly	260	265	270	
Thr	Phe	Phe	Trp	Ser	Val	Val	Ile	Pro	His	Glu	Arg	Arg	Ile	Leu	Thr	275	280	285	
Ile	Leu	Arg	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	Val	Tyr	290	295	300	
Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	Phe	Ser	Gly	His	Lys	Tyr	Gly	Pro	305	310	315	320
Phe	Gly	Pro	Glu	Glu	Ser	Ser	Tyr	Gly	Ser	Pro	Phe	Thr	Pro	Ala	Lys	325	330	335	
Arg	Pro	Lys	Arg	Lys	Val	Ala	Pro	Lys	Arg	Arg	Gln	Glu	Arg	Pro	Val	340	345	350	
Ala	Pro	Pro	Lys	Lys	Arg	Arg	Arg	Lys	Ile	His	Arg	Met	Asp	His	Tyr	355	360	365	
Ala	Ala	Glu	Thr	Arg	Gln	Asp	Lys	Met	Thr	Asn	Pro	Leu	Arg	Glu	Ile	370	375	380	
Asp	Lys	Ile	Val	Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	385	390	395	400
Arg	Arg	Cys	Val	Asn	Val	Ile	Phe	Val	Gly	Asp	His	Gly	Met	Glu	Asp	405	410	415	
Val	Thr	Cys	Asp	Arg	Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	420	425	430	
Asp	Asp	Ile	Thr	Leu	Val	Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	435	440	445	

Phe	Ser	Asn	Asn	Ala	Lys	Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	450	455	460
Thr	Cys	Lys	Lys	Pro	Asp	Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	465	470	475 480
Leu	Pro	Lys	Arg	Leu	His	Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	485	490	495
His	Leu	Leu	Val	Glu	Arg	Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	500	505	510
Val	Tyr	Lys	Lys	Pro	Ser	Gly	Lys	Cys	Phe	Phe	Gln	Gly	Asp	His	Gly	515	520	525
Phe	Asp	Asn	Lys	Val	Asn	Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	530	535	540
Pro	Thr	Phe	Lys	Tyr	Lys	Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	545	550	555 560
Leu	Tyr	Asn	Val	Met	Cys	Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	565	570	575
Asn	Gly	Thr	His	Gly	Ser	Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	580	585	590
Arg	Pro	Thr	Met	Pro	Glu	Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	595	600	605
Met	Tyr	Leu	Gln	Ser	Asp	Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	610	615	620
Val	Glu	Pro	Lys	Asn	Lys	Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	625	630	635 640
Lys	Gly	Ser	Thr	Glu	Glu	Arg	His	Leu	Leu	Tyr	Gly	Arg	Pro	Ala	Val	645	650	655
Leu	Tyr	Arg	Thr	Arg	Tyr	Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	660	665	670
Gly	Tyr	Ser	Glu	Ile	Phe	Leu	Met	Leu	Leu	Trp	Thr	Ser	Tyr	Thr	Val	675	680	685
Ser	Lys	Gln	Ala	Glu	Val	Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	690	695	700

Val Arg Pro Asp Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys Leu
705 710 715 720

Ala Tyr Lys Asn Asp Lys Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro
725 730 735

Tyr Leu Ser Ser Ser Pro Glu Ala Lys Tyr Asp Ala Phe Leu Val Thr
740 745 750

Asn Met Val Pro Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe
755 760 765

Gln Arg Val Leu Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn
770 775 780

Val Ile Ser Gly Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp
785 790 795 800

Thr Glu Asp Lys Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro Val
805 810 815

Pro Thr His Tyr Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln
820 825 830

Pro Ala Asp Lys Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile Leu
835 840 845

Pro His Arg Pro Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu
850 855 860

Ser Lys Trp Val Glu Glu Leu Met Lys Met His Thr Ala Arg Val Arg
865 870 875 880

Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg
885 890 895

Ser Tyr Pro Glu Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu
900 905 910

Ser Glu Ile
915

<210> 70

<211> 979

<212> PRT

<213> Homo sapiens

<220>

<223> Putative autotoxin protein sequence from human liver.

<220>

<221> VARIANT

<222> (860)

<223> Xaa at positions: 860, 889, 905, 911, 927, 937, 944, 950, 954, 967, and 975 represents an unknown or other amino acid.

<400> 70

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp Ile Ser Leu Phe
1 5 10 15

Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg
20 25 30

Ile Lys Arg Ala Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser
35 40 45

Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys Gly Arg Cys Phe
50 55 60

Glu Leu Gln Glu Ala Gly Pro Pro Asp Cys Arg Cys Asp Asn Leu Cys
65 70 75 80

Lys Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys
85 90 95

Thr Ala Arg Ala Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu Val Arg
100 105 110

Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp Cys Leu Ala Arg Gly
115 120 125

Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp
130 135 140

Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Leu Gln Val
145 150 155 160

Cys Ser Pro Ser Ile Asn His Leu Leu Arg Gly Trp Leu Pro Met Thr
165 170 175

Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu
180 185 190

Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	Pro	Thr	195	200	205	
Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	210	215	220	
Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	225	230	235	240
Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly	245	250	255	
Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	Arg	Gly	Glu	Ser	Trp	260	265	270	
Asn	Ile	Leu	Leu	Val	Cys	Cys	His	Pro	Ser	Arg	Ala	Glu	Ile	Leu	Thr	275	280	285	
Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	Val	Tyr	290	295	300	
Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	Phe	Ser	Gly	His	Lys	His	Met	Pro	305	310	315	320
Phe	Gly	Pro	Glu	Met	Thr	Asn	Pro	Leu	Arg	Glu	Met	His	Lys	Ile	Val	325	330	335	
Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	His	Arg	Cys	Val	340	345	350	
Asn	Val	Ile	Phe	Val	Glu	Thr	Met	Asp	Gly	Arg	Cys	His	Met	Tyr	Arg	355	360	365	
Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu	370	375	380	
Val	Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala	385	390	395	400
Lys	Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro	405	410	415	
Asp	Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu	420	425	430	
His	Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu	435	440	445	

Arg	Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro
450						455					460				
Ser	Gly	Asn	Ala	Phe	Ser	Arg	Glu	Thr	Thr	Ala	Phe	Asp	Asn	Lys	Val
465					470					475				480	
Asn	Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr
			485					490						495	
Lys	Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met
		500					505						510		
Cys	Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly
	515					520						525			
Ser	Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro
	530					535					540				
Glu	Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser
545					550					555				560	
Asp	Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn
			565					570						575	
Lys	Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys	Gly	Ser	Thr	Glu
		580					585						590		
Glu	Arg	His	Leu	Leu	Tyr	Gly	Asp	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr
	595						600					605			
Arg	Tyr	Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu
	610					615					620				
Ile	Phe	Leu	Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala
625					630					635				640	
Glu	Val	Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp
				645					650				655		
Val	Arg	Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn
		660						665					670		
Asp	Lys	Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser
	675						680					685			
Ser	Pro	Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro
	690					695					700				

Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu
705 710 715 720

Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly
725 730 735

Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys
740 745 750

Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr
755 760 765

Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys
770 775 780

Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Pro His Arg Pro
785 790 795 800

Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val
805 810 815

Glu Glu Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His
820 825 830

Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu
835 840 845

Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile Xaa
850 855 860

Leu Ser Glu His Leu Gln Tyr Ser Leu Ile Asn Trp Leu Tyr Ile Phe
865 870 875 880

Ile Leu Phe Leu Tyr Leu Leu Ile Xaa Asn Gln Asp Ile Lys Asn Val
885 890 895

Ser Ile Leu Ile Leu Tyr Gln Ile Xaa His Ile Met Pro Glu Xaa Leu
900 905 910

His Cys Phe Ser Leu Met Leu Asp Leu Gly Ser Leu Val Phe Xaa Val
915 920 925

Glu Leu Val Ile Asn Thr Ala Ala Xaa Val Phe Ser Gly Ser Phe Xaa
930 935 940

Met Val Leu Gln Ile Xaa Tyr Leu His Xaa Gly Asn Ile Asn Phe Pro
945 950 955 960

110

7

Met His Ser Cys His Ile Xaa Ser Cys Thr Val Trp Lys His Xaa Phe
965 970 975

Cys Lys Val

DS